

Figure 1.

10080144-022102

201220' 417708001

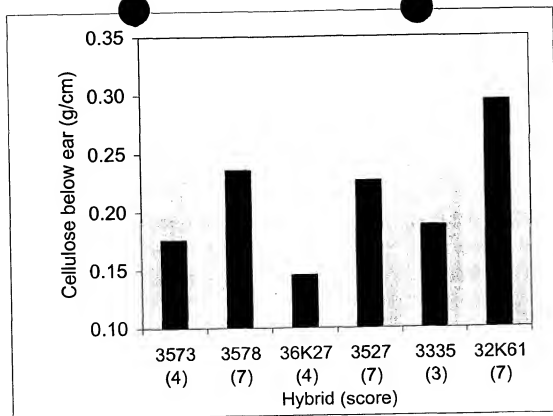


Figure 2

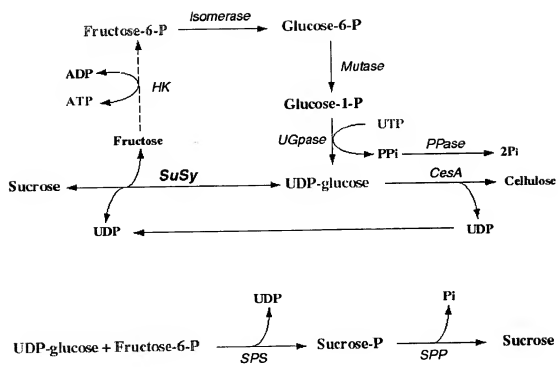


Figure 3.

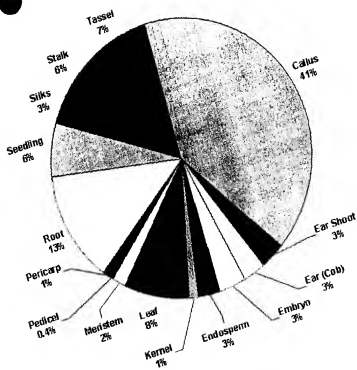


Figure 4.

1008014.022102

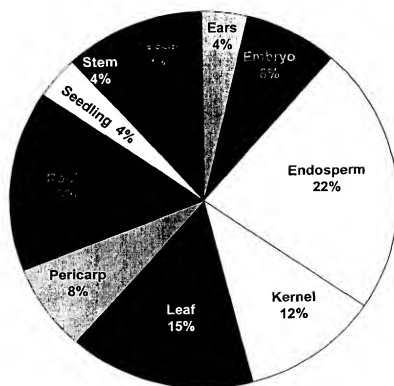


Figure 5

Allele 1: CACC[●]G-mu-AGATTG

Allele 2: CACC-mu-CGGAGATTG

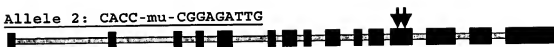


Figure 6.

Figure 7.

Genotype	structural dry matter (% of total dry matter)	cellulose (% of total dry matter)	cellulose (% of structural dry matter)
<i>Sus-1</i> (WT)	63.2	25.2 +/-0.38	39.9
<i>sus-1</i> (mutant)	47.3	17.7 +/-0.34	37.4

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	1	50
Sh1	(1) ----MAAKLTRLHSLRERIGATFSSHPNELIALFSRYVHQGKMLQHQ	
Sus1	(1) MGEAGDRVL SRLHSVRERIGDSL SAHPNELI VAFPTRLKNLKGKGLQHQ	
Sus3	(1) -----STHSAQDRVEDTLHAHRELVALLSKYVNGKGLLQPH	
Consensus	(1) LSRHLSLRERIGDTLSAHPNELVALFSRYVN GKGMLQHQ	
	51	100
Sh1	(46) ILAEFD-ALPDSRKE--KYAPPDTLRAAQEATVLPFWALAIRPRGVK	
Sus1	(51) ITAEYNNAIPEAREKLKDGAFEDVLRAAQEATVLPFWALAIRPRGVK	
Sus3	(41) ILDALDEVQSGGGA-LAGGPELVLRSAQEATVLPFFVATVVRPRGVK	
Consensus	(51) ILAEFD AI DADRE LKDGPFEDVLRAAQEATVLPFWALAIRPRGVK	
	101	150
Sh1	(93) DYIRVNVSELAVEELSVSEYLAFKEQLVDGQSNFNVLLEDFEPFNASFP	
Sus1	(101) EMVRVNVSELAVEELRVPEYLQFKEQLVBEGFPNNFVLEDFEPFNASFP	
Sus3	(89) EMVRVNVHLSVGLTVSEYLRFKBELVDGQHNDPVLLEDFEPFNVSVE	
Consensus	(101) EYVRVNVSELAVEELSVSEYL FKEQLVDGQ N NFVLEDFEPFNASFP	
	151	200
Sh1	(143) RPSMSKSGINGVQFLNRHLSSKLEODKESLYPLINFLKAINYKGTMMLN	
Sus1	(151) RPSLSKSGINGVQFLNRHLSSKLEHDKESLYPLINFLRAHNYKGMTMLN	
Sus3	(139) RPNRSSSGINGVQFLNRHLSSIMFRNRDCLPLDPLFRGHRHKGVMLLN	
Consensus	(151) RPSLSKSGINGVQFLNRHLSSKLF DKESLYPLINFLRAHNYKG TMLN	
	201	250
Sh1	(193) DRIOSLRGLQSLRKAEYYLISVPDTPYSEPNHRFOBLGLEKNGGDTAK	
Sus1	(201) DRIRSLALQALRKAEHHSITLQADTPYSEPHHRFOBLGLEKNGGCAK	
Sus3	(189) DRIOSLRGLQSLTKAEHHSKLPADTPYSOPAYKFOBWSLEKNGGDTAG	
Consensus	(201) DRIOQL ALQSALRKAEHSSLPADTPYSEF HRFOELGLEKNGGDTAK	
	251	300
Sh1	(243) RVLDTLHLLDLLEAPDPANLEKFLGTIPMFNVVILSPHGYFAQSNVLG	
Sus1	(251) RAQETIHLLDLLEAPDPSLEKFLGTIPMFNVVILSPHGYFAQANVLG	
Sus3	(239) HVLEMIHLLDIYQADPDSLEKFLGTIPMFNVVVVSPHGYFGQANVLG	
Consensus	(251) RVLETIHLLDLLEAPDPSTLEKFLGTIPMFNVVILSPHGYFAQANVLG	
	301	350
Sh1	(293) YPDTCGGQVVYILDQVRALENEMLLRIKQGLDITPKILIVTRLIPDAAGT	
Sus1	(301) YPDTCGGQVVYILDQVRAMENEMLLRIKQGLDITPKILIVTRLIPDATGT	
Sus3	(289) LPDTCGGQIVYILDQVRALENEMVLRLLKQGLDVSPPKILIVTRLIPDAKGT	
Consensus	(301) YPDTCGGQVVYILDQVRALENEMLLRIKQGLDITPKILIVTRLIPDA GT	
	351	400
Sh1	(343) TCCQRLEKVGTEHTDITRVFFRNENGILRKWISRFDVWPYLETYTBDVS	
Sus1	(351) TCCQRLEKVLGTEHCHILRVFFRTENGIRKWKISRFEVWPYLETYTDDVA	
Sus3	(339) SCNQRLEIRISGTHYILRVFFRNENGILKWKISRFDVWPYLETBABDAA	
Consensus	(351) TCCQRLEKVGTEHTHILRVFFRNENGILRKWISRFDVWPYLETTYTEDVA	
	401	450
Sh1	(393) SETMKENQAKPDLITIGNYSDGNLVATLAAHKLVGTCTIAHALEKTKYPN	
Sus1	(401) HETAGELQANPDLITIGNYSDGNLVACLAAHKVGVTCTIAHALEKTKYPN	
Sus3	(389) GETAABLQGTDPDLITIGNYSDGNLVASLLSYKMGITQCNIAHALEKTKYPD	
Consensus	(401) ETAAELQA PDLITIGNYSDGNLVASLAAHKMGVGTCTIAHALEKTKYPN	
	451	500
Sh1	(443) SDIYLDKFD SQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDVTGOYE	
Sus1	(451) SDLYWKKFEDHYHFSCQFTADLIAMNHADFIITSTFQEIAGNKDVTGOYE	
Sus3	(439) SDIFWNKFEKHYHFSCQFTADLIAMNHADFIITSTYQEIAGSKNVTGOYE	
Consensus	(451) SDIYWKKFDD YHFSCQFTADLIAMNHADFIITSTFQEIAGSKDVTGOYE	
	501	550
Sh1	(493) SHIAFTLPGLYRVVHGIDVDFDPKFNI VSPGADMSVYYPYTETDKRLTAFH	
Sus1	(501) SHMAFTMPGLYRVVHGIDVDFDPKFNI VSPGADLSYFPYTESHKRLTSLH	
Sus3	(489) SHTAFTLPGLYRVVHGIDVDFDPKFNI VSPGADMSIYFPYTESKAKRLTSLH	
Consensus	(501) SHTAFTLPGLYRVVHGIDVDFDPKFNI VSPGADMSIYFPYTES KRLTSLH	

Figure 8a

551 600

Sh1 (543) PETEELIYSDVENSEHKKFVLKDKKKPTIFSMARLDRVKNMTGLVEMYGKN
 Sus1 (551) PETEELIYSQTEHTEHKKFVLNDRNKPITFSMARLDRVKNLTGLVEDIYGRN
 Sus3 (539) GSTENLIYDPEQNDHIGHLDNRKPIILFSMARLDRVKNITGLVSAFAKC
 Consensus (551) PETEELIYS ENSEHKKFVL DR KPIIFSMARLDRVKNITGLVLEYGKN

601 650

Sh1 (593) ARRLRELNLVIVAGDHGK-ESKDREEQAEFKKMYSLIDYKIKGHIRWIS
 Sus1 (601) KRLCELNLVNVVCGDHGN-PSKDKKEQAEFKKMPDLIEQYNLNGHIRWIS
 Sus3 (589) AKRLRELNLVNVVAGYNDVNKSKDREETARIEKMHELITKTNLFCQFRWIS
 Consensus (601) ARRLRELNLVNVVAGDHG SKDREEQAEFKKMHLID YNL GHIRWIS

651 700

Sh1 (642) AQMNVRNGELRYRICDTKGAFVQPAFYEAFLTVIESMTGCLPTATCH
 Sus1 (650) AQMNVRNGELRYRICDTKGAFVQPAFYEAFLTVIEAMTCGLPTATAY
 Sus3 (639) AQMNVRNGELRYRICDTKGAFVQPAFYEAFLTVIEAMTCGLPTATLH
 Consensus (651) AQMNVRNGELRYRICDTKGAFVQPAFYEAFLTVIEAMTCGLPTAT H

701 750

Sh1 (692) GGPAEIIIVHGVSGLHIDPYHSDKAADTLVNFDDKCKADBSYWDEISQGGI
 Sus1 (700) GGPAEIIIVHGVSgyHIDPYQGDKASALLVDFFDKCOAEBSHWSKISQGGI
 Sus3 (689) GGPAEIIIEHGVSGFHIDPYHPEQAVNLMDFFDRCKODEHWNVSQAGI
 Consensus (701) GGPAEIIIVHGVSGFHIDPYH DKAA LLVDFFDRCKADPSHW ISQGGI

751 800

Sh1 (742) QRIYEKYTWKLYSERIMTLTGvyGFWKYVSNLRRRETRRYLEMFLYALKYR
 Sus1 (750) QRIEKEYTWKLYSERIMTLTGvyGFWKYVSNLRRRETRRYLEMFLYALKYR
 Sus3 (739) QRIYEKYTWKLYSERIMTLTGvyGFWKYVSKLRLERTRRYLEMFLYALKYR
 Consensus (751) QRIYEKYTWKLYSERIMTLTGvyGFWKYVSNLRRRETRRYLEMFLYALKYR

801 817

Sh1 (792) SLASTVPLAIDSPD-----
 Sus1 (800) TMASTVPLAVEGEPSK
 Sus3 (789) ELASTVPLAID-OPQ--
 Consensus (801) SLASTVPLAID P

Figure 8b

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Sh1 (1) AAACCCCTCCCTCCCTCCATTGGACTGCTTGCCTCTGTTGACCATG 50
Sus1 (1) -----GCTCTAG-GATCCAGGAAGGACG 50
Sus3 (1) -----
Consensus (1) ----- G CTG G TCC G GA A G
51 100
Sh1 (51) GGTATTCTGAACCACTGAGCCATGGCTGCAAGCTGACTGCCCTTCACAG 100
Sus1 (26) CA-ATGGGGGAGGCTGAGGTGACCGTGTCTCTGAGCGCCCTCCACAG 100
Sus3 (1) -----GTCCAG-CCACGC 100
Consensus (51) AT G A T AG TG C CTGAGTGGCTCCACAG 100
101 150
Sh1 (101) TCTTCGCGAAGCGCTTGGTGCACCTTCTCTCTCCCATCCCAATGAAGCTGA 150
Sus1 (72) CGTCAGCGGAGCGGATTTGGCGACTGACTCTCTGCCCACCCCAATGAGCTTG 150
Sus3 (13) GTCCGCGAAGCGGCTGAGGACACCTTCAAGCGGACCGCAAGGAGCTG 150
Consensus (101) TC GCGA CGC TTGG GACACCTCTCGGCCACCCCAATGAGCT G 150
151 200
Sh1 (151) TAGCACTCTTTTCCAGGATATGTCACCAAGGCAAGGGAATGCTTCAGCGG 200
Sus1 (122) TCGCGCTCTTACCCAGGCTGAAACACTTGGAAAGGGTATGCTGCAGGCC 200
Sus3 (63) TCGCCCTCTTCTCCCAAGTACGTGAACAAGGGGAAGGGCATCTCTGCAGCG 200
Consensus (151) TCGCCCTCTT TCCAGGTA GT AACCAGG GAGGG ATGCTGCAGGCC 200
201 250
Sh1 (201) CATCAGCTGCTTCGCGAGTTTGA---TGC---CCTGTT--TGATAGTGA 250
Sus1 (172) CACCAGATCATTTGCCGAGTACAACAATGCGATCCTGTAGGCTGAGCGCGGA 250
Sus3 (113) CACCACTCTCTGACGCGCTGACGAGGT---CGAGG-CTCCGGGGG 250
Consensus (201) CACCAGATCCTTGCGAGTTGCGAC ATGC CCTG G CTGAG G GA 250
251 300
Sh1 (242) CAAGGAGAA--TATGCACCAATTGAAGACATCTTCGTGTGCTCAGGA 300
Sus1 (222) GAAGCTCAAG--GATGGTGTCTTTGAGGATGTCTGTAGGGGAGCTCAGGA 300
Sus3 (158) GCGCGGTAGCCGAGGACCTTCTCGACCTCTCGCTGCGCGAGGA 300
Consensus (251) CAAGC CAAG GATGGACC TTTGA GACGTCT CG GC GCTCAGGA 300
301 350
Sh1 (290) AGCAATTGTGCTCCCCCATGGGTTGCACTTGCTATCAGGCCAAGGCTG 350
Sus1 (270) GCGGATTTCTCATCCCCCATGGGTTGCACTTGCCATCGCCCTAGGCGCTG 350
Sus3 (208) GCGGATTTGTGCTCGCGCGGTTCTGTGGCCTCGCGTGGCGCGCGCGG 350
Consensus (301) GCGGATTTGTGCTCCCCCATGGGTTGCACTTGCT ATCGGCC AGGCGT 350
351 400
Sh1 (340) GTGTCTGGGATTAATTTCCGGTGAAATGTAAGTGAGCTGGCTGTGGAGGAG 400
Sus1 (320) GTGTCTGGGAGTATGTGAGGTCACGTCAGTGAGCTCGCTGTTCAGGAG 400
Sus3 (258) GAGTTTCGGAGTACGTCCGCTCAACGTTACGAGCTGAGCTGAGGAG 400
Consensus (351) GTGTCTGGGAGTACGT CCGGTCACGCT AGTGAGCTCGCTGT GAGGAG 400
401 450
Sh1 (390) CTGAGTCTTTCTGAGTACTTGGCAATCAAGGAACAGCTGGTGGATGGAC 450
Sus1 (370) CTGAGAGTTCTGAGTACCTGCGAGTTCAAGGAACAGCTTTGGGAAGAAGG 450
Sus3 (308) CTCAAGTCTCGGAGTACCTCGGCTTCAAGGAGGAGCTTGTGCAAGGCG 450
Consensus (401) CTGAGAGTTTCTGAGTACCTGC TTCAAGGAACAGCTTTGTGA GGACA 450
451 500
Sh1 (440) ATCCAAACGCAACTTTGTGCTTGAGCTTGATTTTGAGCGCTTCAATGCT 500
Sus1 (420) CCCCAACAACTTTGTTCTTGAGCTTGAGCTTTGAGCCATCAATGCT 500
Sus3 (328) GCACAAATGATCTTACGTTCTGAGCTTGACTTCGAGCGCTTCAATGCT 500
Consensus (451) CCCCAACAACTTTGTTCTTGAGCTTGAGCTTTGAGCC TTCAATGCT 500
501 550
Sh1 (490) CTTTCTCTGCTCTTCATGTGCAAGTCCATCGGAATGGAATGCAATTC 550
Sus1 (470) CTTTCTCTGCTCTCTCTGCAAGTCCATGGCAATGCTGTGAGTTG 550
Sus3 (408) GATTCCTGCGCTCAATCGGTATCATCTATTTGGAATCGGTGCAATTC 550
Consensus (501) CTTTCTCTGCTCTCTGCAAGTCCATGGAAATGG GTGCAATTC 550

Figure 9a

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		551	600
Sh1	(540)	CTTAACCGACACCTGTGCTCAAGTTGTTCCAGGACAAGGAGAGTTTGTA	
Sus1	(520)	CTCAAGAGGCACCTGTGATCAAAAGCTCTCCATGACAAGGAGAGGATGTA	
Sus3	(458)	CTCAACCGACACCTGTGCTCAATCATGTTCCGCAACAGGGATTGCTTGGA	
Consensus	(551)	CTCAACCGACACCTGTGCTCAAG TGTCCA GACAAGGAGGCTTGTA	
		601	650
Sh1	(590)	CCCCCTTGCTGAACCTTCCTCAAGGCTCATAACTACAAGGGACGAGCATGA	
Sus1	(570)	CCCCCTTGCTCAACTTCCTTCGCGCCCAACAACATAAGGGGATGACATGA	
Sus3	(508)	CCCCCTGTTTGATTTCCCTCCGTGGCCACCGGCACAAGGGGCTGTTTATGA	
Consensus	(601)	CCCCCTTGCTGAACTTCCTCCG GCCACAACATAACAAGGGGA GAC ATGA	
		651	700
Sh1	(640)	TGTTGAATGACAGAATCCAAAGCCTTCGTGGTCTCCAACTCATCTCTGAGA	
Sus1	(620)	TGTTGAACGACAGAATCCGCAGCTCTCAAGTCTCTGCAAGGTGCGCTGAGG	
Sus3	(558)	TGCTTAATGATAGAATACAAAGCTTGGGGAGGCTTCAGCTCTGCTCTGACC	
Consensus	(651)	TGTTGAATGACAGAATCCAAAGCCT GTGGTCT CAATCTCGCGTGAG	
		701	750
Sh1	(690)	AAGGCTAGAGGAGTATCTACTGTGTCTCTCAAGACACTCCCTACTCGGA	
Sus1	(670)	AAGGCTAGGAGGACCTGTCCACCTAGAAAGCTGATACCCATACTCTGA	
Sus3	(608)	AAGGCTAGGAGGACATCTCTCAAGCTCCCTGTGACACACCATACTCAAC	
Consensus	(701)	AAGGCTAGGAGGACCTGTGCT A CT CCGTGTGACAC CCATACTC GA	
		751	800
Sh1	(740)	GTTCACCATAGGTTCCAAGAGCTTGGCTTGGAGAAGGGTTGGGGTGAC	
Sus1	(720)	ATTTCACCAAGCTTCCAGGACTTGGCTCTGGAGAAGGGTTGGGGTGATT	
Sus3	(658)	ATTTCGCTTATTAATTTCAAGAGTGGGGCTGGAGAAGGTTGGGGTGATA	
Consensus	(751)	ATTT ACCATAGGTTCCAAGAGCTTGGCTGGAGAAGGGTTGGGGTGATA	
		801	850
Sh1	(790)	CTCCGAAGCGTGTCTCTGACACACTCCACTGCTTCTCGACCTCTCTGAG	
Sus1	(770)	GCGCTAAGCGTGCAGAGGACACTATCCACCTCTCTCTGACCTCTCTGAG	
Sus3	(708)	GAGCAGGACATGTTTGGAAATGATCCATCTCTCTAGACATCATTCAG	
Consensus	(801)	C GC AAGCGTGTCTGGA AC ATCCACCTCCTTCT GACCTCTCTGAG	
		851	900
Sh1	(840)	GCCCCGATCCCTGCCAAGTTGGAGAACTTCCCTGGAACTATACCAATGAT	
Sus1	(820)	GCCCCAGATCCCTCCACCTGGAGAACTTCCCTGGAAAGATCCCATGCT	
Sus3	(758)	GCCCCAGATCCATCTATCCCTAGAGAAATCTTGGGGAGGATCCCATGAT	
Consensus	(851)	GCCCCAGATCC TCCACCTGGAGAACTTCCCTGGAAAGATCCCATGAT	
		901	950
Sh1	(890)	GTTCAACGTTGTTATCCTGTCTCTCATGGCTACTTCCGCCAGTCTCAATG	
Sus1	(870)	GTTCAAGTGTCTTATCCTCTCCCTCATGGTTACTTCGCTCAAGCTAATG	
Sus3	(808)	TTTAAAGTTGTTGGGTTATCCCTCATGGATACTTTGCTCAAGCTAATG	
Consensus	(901)	GTTCAACGTTGTTATCCT TCCCTCATGG TACTTCGCTCAAGCTAATG	
		951	1000
Sh1	(940)	TCCTTGATACCTCTGACACTGCGCTCAGGTTGTGTACATTTCTGATCAA	
Sus1	(920)	TCCTTGATACCTCTGACACCGAGGCCAGGTTGTCTACATCTTGATCAA	
Sus3	(858)	TATTAGCTTTCGACACACAGGAGACAGATCGTCTATATATCTGAGCCAA	
Consensus	(951)	T TT GG TACCCTGACAC GGAGG CAGGTTGTCTACAT CTGGATCAA	
		1001	1050
Sh1	(990)	GTCCGCTGTTTGGAGAAATGAGATGCTTCTGAGGATTAAGCAGCAAGGCTT	
Sus1	(970)	GTCCGCTGTTTGGAGAAATGAGATGCTTCTGAGGATTAAGCAGCAAGGCTT	
Sus3	(908)	GTCCGCTGATTAAGAAATGAGATGCTTCTCTGTTTAAAGAAACAAGGCTT	
Consensus	(1001)	GTCCGCTGCT TGGAGAAATGAGATGCTTCTGAGGAT AAGCAGCAAG CT	
		1051	1100
Sh1	(1040)	TGATATCACTCCGAAGATCTCTATTGTTACCAAGGCTGTTCCCTGATGGTG	
Sus1	(1020)	TGATATCAAGCCGAAGATCTCTATTGTTACCAAGGCTGTTCCCTGATGGCA	
Sus3	(958)	TGATGTTTCCCAAAGATTCTCAATTGTTACTCGGCTGATACAGATGCAA	
Consensus	(1051)	TGATATCAC CCGAAGATCTCTATTGTTACCAAGGCTG T CCTGTGACAA	

Figure 9b

		1101		1150
Sh1	(1090)	CTGGAGATAGCTGGCTCAGCGGCTGGAGAAGGTCATTGGTACTGACAC		
Sus1	(1070)	CTGGACACCACTTTGGCGTACGCGCTTGAGAAGGTCCTTGGCACCAGGAC		
Sus3	(1008)	AAGGAACATATGGAATCAAGCGCTTGAGAAGTAATTAGTGGAACACACCAT		
Consensus	(1101)	CTGG AC AC TGGCGTACGCGCTTGAGAAGGTCATTGG AC GAGCAC		
		1151		1200
Sh1	(1140)	ACAGACATCATTCGCGTTCCCTTCAGAAATGAGATGGCATCTCCGCA		
Sus1	(1120)	TGCCATATCTTCGCGTGGCTTCAGAAACAGAAACGGAATCTTCGCAA		
Sus3	(1058)	ACTTACATATACGAGTTCCCTTCAGAAATGAAATGGGATCTTAAAGA		
Consensus	(1151)	AC ACATC TTGCGGTTCCCTTCAGAAATGAAATGG ATCTTTCGAA		
		1201		1250
Sh1	(1190)	GTGGATCTCTCGTTTGTATGCTCGGCATACCTGGAGACATACACTGAGG		
Sus1	(1170)	GTGGATCTCGGATTGTGAATCTCGCGTACCTGGAGACTTACACTGATG		
Sus3	(1108)	ATGGATATCAAGATTGTATGTGTGGCCATATCTGGAAACATTTGTGAGG		
Consensus	(1201)	GTGGATCTC CGATTGTATGCTCGGCATACCTGGAGACATACACTGAGG		
		1251		1300
Sh1	(1240)	ATGTTTCCAGTGAATAATGAAAGAAATGACAGGCCAAACCTGACCTTATC		
Sus1	(1220)	ACGTGGCGCATGAGATTGCTGGAGAGCTTCAGGCCAATCTGACCTGATC		
Sus3	(1158)	ATGCTGTGTGGTGAATTTGCTGTGAATACAAAGTACTCCAGAGACTTATA		
Consensus	(1251)	ATGTTGC GTGAATTTGCTG AGAA T CAGGCCAATCTGACCT ATC		
		1301		1350
Sh1	(1290)	ATTGGCAACTACAGCGATGGCAACCTAGTCTGCACTCTGCTCGCGCACAA		
Sus1	(1270)	ATCGGAAACTACAGTGACGGAACCTTTGTCGTGTTTGTCTCGGCCACAA		
Sus3	(1208)	ATTGGAAACTACAGTATGGAATTTGTGGCGTCAATGCTATCTTACAA		
Consensus	(1301)	ATTGGAAACTACAGTGATGGAACCTTTG CGCTCTTTGTCTGC CACAA		
		1351		1400
Sh1	(1340)	GTTGGGAGTCACTCAGTGATACCTGCTCATGCTCTGGAGAAACCAAAAT		
Sus1	(1320)	GATGGGTGTTACTCACTGTACCATTTGCCATGCGCTTGAGAAAACTAAGT		
Sus3	(1258)	GATGGGAATTACCCAGTGCAACATTGCTCTATGCTCTGGGAAAGCACTAAGT		
Consensus	(1351)	GATGGGAGTTACTCAGTGATACCATTTGCTCATGC CTGGAGAAAACTAAGT		
		1401		1450
Sh1	(1390)	ACCCAACTCGGACATCTACTTGGACAAATTCGACAGCCAGTACCACCTTC		
Sus1	(1370)	ACCCTAACCTCGACCTCTACTGGAAGAACTTTGAGGATCACTACCACCTTC		
Sus3	(1308)	ATCCAGATTGACACATATTTTGGGAAGAAATTCGATGAGAAGTACCATTTC		
Consensus	(1401)	ACCC AACTC GACATCTACTGGAAGAA TTCGA GA CAGTACCACCTTC		
		1451		1500
Sh1	(1440)	TCCTGGCCAGTTCAAGCTGACCTTATTGGCATGAACCAACCCGATTTTCAT		
Sus1	(1420)	TCGTGCGAGTTCAACCACTGACCTTGAATTGCAATGAACCATGCCGACTTCAT		
Sus3	(1358)	TCCTGGCCAGTTCACTGCTGATATATTTGCTATGAACAATGCTGATTTCAT		
Consensus	(1451)	TC TGGCCAGTTCACT GCTGAC T ATTGC ATGAACCATGCCGATTTCAT		
		1501		1550
Sh1	(1490)	CATCACCAGCACATTCCAAGAAATGCGGGAAGCAAGGACACCGTGGGGC		
Sus1	(1470)	CATCACCAGTACCTTCCAAGAGATCGCGGAAGCAAGGACACCGTCGGCC		
Sus3	(1408)	CATCACCAGCACATCCAAGAAATGCTTGAAGCAAAATATGCTTGGAC		
Consensus	(1501)	CATCACCAGCACATTCCAAGAAATGCG GGAAGCAAGGACACCGT GG C		
		1551		1600
Sh1	(1540)	AGTACGAGTCCATATCGGTTACACTCTTCTGGCTCTACCGTGTGCTC		
Sus1	(1520)	AGTACGAGTCAACATGGCTTCACAAATGCCTGGCTGTACCGGCTGTGTC		
Sus3	(1458)	AGTATGAGAGTCATATGGCTTACTCTGCTGGCTGTATGACCGAGTTGTC		
Consensus	(1551)	AGTACGAGTC CATAT CGCTTCACTCTGCCTGS CTGTACCG GTTGC		
		1601		1650
Sh1	(1590)	CATGGCATCGATGTTTTCGATCCCAAGTTCAACATGTCTCTCTCTGGAGC		
Sus1	(1570)	CACGGCATGTATGTTTCGACCCCAAGTTCAACATGTCTCTCTCTGGCGC		
Sus3	(1508)	CATGGCATCGATGTTTCGATCCCAAGTTCAACATGTCTCTCTCTGGAGC		
Consensus	(1601)	CATGGCATCGATGT TTCGATCCCAAGTTCAACAT GTCTCTCTCTGGAGC		

Figure 9c

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		1651		1700
Sh1	(1640)	AGACATGAGTGTTTACTACCCCTATACGGAACCGACAAGAGACTCACTG		
Sus1	(1620)	GGACCTGTCCATCTACTTCCGCTACACGAGTCGCAACAAGAGGCTGACCT		
Sus3	(1558)	TGACATGTCCATATACTTTCACATACCGAGAGGCCAAGCGACTACCT		
Consensus	(1651)	GACATGTCCAT TACTCCC TATACCGAGACGGAACAAGAGACTCACCT		
		1701		1750
Sh1	(1690)	CCTTCCATCTCGAAATCGAGGAGCTCATCTACAGGCACTCGAGAACTCC		
Sus1	(1670)	CCCTTCCACCGGAGATTGAGGAGCTCTGTACAGCCAAACCGAGAACAGG		
Sus3	(1608)	CTCTTCATGGTTCAATCGAAATTTGATTTATGACCCCGAGCAAAACGAT		
Consensus	(1701)	CCCTTCATCTCGAAATCGAGGAGCTCAT TACAGCCA C GAGAGAC C		
		1751		1800
Sh1	(1740)	GAGCACAAAGTTCTGTTCTGAAGCAGCAAGAGCGATCATCTTCTCGAT		
Sus1	(1720)	GAGCACAAAGTTCTGTTCTGAAGCAGCAAGCAATCATCTTCTCCAT		
Sus3	(1658)	GACACATTGGGCACTGTGATGACGGTCAAGCGCATCTCTTCTCCAT		
Consensus	(1751)	GAGCACAAAGTTCTGTTCTGAAG CACAGGAA AAGCC ATCATCTTCTCCAT		
		1801		1850
Sh1	(1790)	GGGCGCTCTCGACCGCGTGAAGAACATGACAGGCTTGGTCGAGATGTGAT		
Sus1	(1770)	GGCTCGTCTCGACCGGTGTGAAGAAGTTGAGTGGCTGGTGGAGCTGTACG		
Sus3	(1708)	GGCAAGATCGAGAGGCTGAAGAACATTAACAGGGCTGGTCGAGAGCTTTTG		
Consensus	(1801)	GGC GCTCTCGACCG GTGAAGAACATGACAGGGCTGGTCGAG TGTACG		
		1851		1900
Sh1	(1840)	GCAAGAACCGCGCGCTGAGGAGCTGGCAACCTCGTATCGTTGGCGGT		
Sus1	(1820)	GCCGGAACAAGCGGCTGACGAGCTGGTGAACCTCGTGGTCTGTGCGGC		
Sus3	(1758)	CTAAGTCGGCTAAGCTGAGGAGCTGGTAACCTTGTCTGCTGTGCGCGG		
Consensus	(1851)	GCAAGAACCGCGGCTGAGGAGCTGGTGAACCTCGTGGTCTGTGCGGC		
		1901		1950
Sh1	(1890)	GACCAAGG---CAAGGAGTCCAAGGACAGGAGGAGCAGGCGGAGTTCAA		
Sus1	(1870)	GACCATGG---CAACCTTCCAAGGACAGGAGGAGCAGGCGGAGTTCAA		
Sus3	(1808)	TACAATGATGTCAACAGTCCAAGGACAGGGAAGATTCGCGGAGATAGA		
Consensus	(1901)	GACCATGG CAAC AGTCCAAGGACAGGAGGAGCAGGCGGAGTTCAA		
		1951		2000
Sh1	(1937)	GAAGATGTACAGCCTCATCGACGAGTACAACTGAAAGGCGCATATCCGCT		
Sus1	(1917)	GAAGATGTTTGACCTCATCGAGCAGTACAACTTGAACGGGCACATCCGCT		
Sus3	(1858)	GAAGATGCATGAATCATCAAGCCCAACAACCTGTTCCGGCAGTTCGCGCT		
Consensus	(1951)	GAAGATGTATGACCTCATCGAG AGTACAACTTGAACGGGCA ATCCGCT		
		2001		2050
Sh1	(1987)	GGATCTCGGCGCAGATGAACCGCTTCCGCAACGGCGAGCTGTACCGCTAC		
Sus1	(1967)	GGATCTCCGCCAGATGAACCGCTTCCGCAACGGCGAGCTGTACCGCTAC		
Sus3	(1908)	GGATCTCTGCCAGACAAAGAGGCGCCGTAACGGCGAGCTGTATCGCTAC		
Consensus	(2001)	GGATCTC GCCAGATGAACCG GTCCGCAACGGCGAGCTGTACCGCTAC		
		2051		2100
Sh1	(2037)	ATTTCGATACCAAGGGCGCATTCGTGAGCCTGCGTTCTACGAAGCGTT		
Sus1	(2017)	ATCTGCGACACCAAGGCGCGCTTCGTGAGCCTTGGTTTCTACGAAGCGTT		
Sus3	(1958)	ATCGCTGATACCCATGTTGTTTCTGTAACGCGCGCTTGTATGAAGCGTT		
Consensus	(2051)	ATCTGCGATACCAAGGGCGC TCTGTGAGCCTGC TTCTACGAAGCGTT		
		2101		2150
Sh1	(2087)	CGGCTGAGTGTGATCGAGTCCATGACGTGCGGCTCTGCCAACGATCGCGA		
Sus1	(2067)	CGGCTGAGGTTGGTTGAGGCCATGACCTGCGGCTGCCCAAGTTCGCGA		
Sus3	(2008)	CGGTCTACCGCTGTTGAGGCCATGACCTGCGGCTTCTGATTTTCGCGA		
Consensus	(2101)	CGG CTGAC GTGTTGAGGCCATGACCTGCGG CTGCC ACGTTTCGCGA		
		2151		2200
Sh1	(2137)	CTGCTCATGGCGGCGCTCTGAGATCATCGTGGACGGGATATCTGGGCTG		
Sus1	(2117)	CCGCTACGGCGGCTCGGCTGAGATCATCGTGCACGGGCTGTCTGGCTAC		
Sus3	(2058)	CGCTCCATGGAGTCCAGCTGAGATCATAGCAATGGGCTCTCGGCGTTG		
Consensus	(2151)	CC CCATGGCGGTCC GCTGAGATCATCGTGCACGGGCT TCTGGCTTC		

Figure 9d

		2201		2250
Sh1	(2187)	CACATTGACCCCTTACCACACGGACAAGGCGGGATATCTCGGTGAACCTT		
Sus1	(2167)	CACATCGACCCCTTACCAGGCGGACGAGCCACTGGAGCAAGATCTCCAGG		
Sus3	(2108)	CACATTGACCCGTACCACCCGGAACAGGCTGTTAATCTGATGGCGCACTT		
Consensus	(2201)	CACATTGACCCCTTACCAC GCGACAAGGC GGGATCTGCTGGTGCACCTT		
		2251		2300
Sh1	(2237)	CTTTGCAAAATGCAAGGCAGATCTCGAGTACTGGGACGAGATCTCAACGG		
Sus1	(2217)	CTTCGACAAGTGCCAGGCGGAGCCGAGCCACTGGAGCAAGATCTCCAGG		
Sus3	(2158)	CTTCGACCGGTGCAAGCAAGACCCAGATCTCTGGTGAATATATCTGGAG		
Consensus	(2251)	CTTCGACAAGTGCAAGGCAGA CCGAGCCACTGG CAAGATCTC CAGG		
		2301		2350
Sh1	(2287)	GCGGCTGCGACAGAAATTTATGAGAAGTACACCTGGAAGCTCTACTCTCGAG		
Sus1	(2267)	GCGGGCTCCAGCGTATCGAGGAGAAGTACACCTGGAAGCTGACTCTGGAG		
Sus3	(2208)	CAGGGCTGACGCGCATATACGAGAAGTACACATGGAAGATATATCTGAGAG		
Consensus	(2301)	GCGGGCTGACGCG AT TA GAGAAGTACACCTGGAAGCT TACTC GAG		
		2351		2400
Sh1	(2337)	AGGCTGATGACCCCTGACCGGCGTGTACCGGGTCTCGGAAGTACGTGAGCAA		
Sus1	(2317)	AGGCTGATGACCCCTCACC GGCGTGTACCGGTCTCGGAAGTACGTGTCCAA		
Sus3	(2258)	AGGTTGATGACACTGGCCGGGTCTACCGGTTCTCGGAAGTACGTGTGCAA		
Consensus	(2351)	AGGCTGATGACCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGTCCAA		
		2401		2450
Sh1	(2387)	CCTGGAGAGGCGCGAGACCCGCGCTACATCGAGATGTTCTACGGCTCGA		
Sus1	(2367)	CCTGGAGAGGCGCGAGACCCGGCGGTACTCGAGATGTTCTACGGCTCGA		
Sus3	(2308)	GCTCGAGAGGCTGGAGACGAGCGCTACCTTGAGATGTTCTACATCTCGA		
Consensus	(2401)	CCTGGAGAGGCGCGAGACCCGGCGCTACCT GAGATGTTCTACGG CTGA		
		2451		2500
Sh1	(2437)	AGTACCGTAGCTTGGCAAGCCAGGTTCCGCTGTCTCTCGA-----TTAG		
Sus1	(2417)	AGTACCGCAACATGGCGAGACCCGTGCGCTGGCGCTGGA-----GGGA		
Sus3	(2358)	AGTTCGGCGAGCTGGCGAGACCCGTGCCGCTTGGAAATGACCAACCCGAG		
Consensus	(2451)	AGTACCGCA CTTGGCGAGACCCGTGCCGTGCCC T GA G AG		
		2501		2550
Sh1	(2481)	TTCGGGGAAGAAAGGAGAAAGAAAGCAAGAGCCAGGCGCGGA-----G		
Sus1	(2461)	GAGGCTTCAGCAAGTGA-TGCGTGAAGCGGCGCAAGAGCTGATC-----G		
Sus3	(2408)	TAGGTTGGCAACTGCGACTCGGTAAGCACTTGATACAGACTGAACAACCTG		
Consensus	(2501)	TAGC GC AGAA G GA TGGCTAACA GGCACAGGCTGA G		
		2551		2600
Sh1	(2525)	AACCATGCGCTGCATTTCTGATCT-----GT-TTCACCCCAATTTCG		
Sus1	(2507)	ATCGATGAGCGAGAGGGAGCACTCGGA-----GT-GTGGTGTTTTCG		
Sus3	(2458)	AAGGACCTTCAGTAATTTAGCGCGCGCAGACGTTAGCAGATAAATGTGC		
Consensus	(2551)	AACGATC C G A TT G CTCGG GT GTCA CAATTTCG		
		2601		2650
Sh1	(2565)	ATTGTTAGTCTGTGATTTGGAGTTATGTG--TACTTGGTTTCAGAGACTT		
Sus1	(2551)	TTGCCATTTCTTTCTTTCTTTCTTTTC--TTCCCGGAGGCGAAATAAA		
Sus3	(2508)	CCGAGCTGAACCTGTTTTTTATTATGTACATATGGCAGATATACAAAT		
Consensus	(2601)	TG TGTC TG TTT TT TTATGT TACT GGAGTC AA AAAAT		
		2651		2700
Sh1	(2613)	TGTTTCTTCTCGTTTCTTTCTTTCTTTGTTTGAAGCTTTTGGGAGCGCTG		
Sus1	(2599)	AGACTC-TGCTT-TTGCTAGCGGCGGCGCTTCTGTTCTGCTGTTTCTCT		
Sus3	(2558)	TACTGAAGCAGGTGGGTTGCAGTTGTGTGTCTGTTACTG-----TT		
Consensus	(2651)	TG TTC TGCT GTTG TTG CGTTGTGTGTGCTT CTG C GCTT		
		2701		2750
Sh1	(2663)	GCTTGTTCTTCTAGTATGTTGGAAATGGCTGCACCTTTGCTTGCATATAT		
Sus1	(2647)	CAAGATTAATAATTTACCTACC--TTGCTAAGGTCTCTTCTCATCATTT		
Sus3	(2600)	TACTGTATATGTCAGCTGTC--GGCTGCATATTTCTTGCTGC--CA		
Consensus	(2701)	ACTGGTTT ATATTAAAGTC C TTGGCTGCA CTT TTC TGA T A		

Figure 9e

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                2751                                2800
Sh1 (2713) AAATGCCTGCTCGTTACCTTGCTTCCAGAGTGC-----
Sus1 (2695) TCCGGGTGTGCTTTGTAGTAGTCTGATGGACTGTTAGTAGTTTGCCTTGC
Sus3 (2644) AGCCCGGAGGCACTGGTGAAGTCTGATAAATACATCATATTTCTTTGACC
Consensus (2751) A C GC GGC CTTGTA GTCTGATAGA TG T TA T TG C
                2801                                2850
Sh1 (2747) -----
Sus1 (2745) GTCGGTTGAGAGGGAAACGTTGGTGGTGGTGGTGTGTGTGCAGTCAGGCGT
Sus3 (2694) TGTGAAAAAATAAAAAAAAAAAAAAAAAAAAAAGGCGCCCG-----
Consensus (2801) G A A AA G G G C

                2851                                2900
Sh1 (2747) -----
Sus1 (2795) GGTGCTCCCTTTGTTTCCTGGATGGGATGTTGCTCCTTGAATAATAATCG
Sus3 (2738) -----
Consensus (2851)

                2901                                2950
Sh1 (2747) -----
Sus1 (2845) TAGTGGCCTTGGAGCCCTTTTCCTGAAATAAGAGCAGCATCCTAGTGCCT
Sus3 (2738) -----
Consensus (2901)

                2951                2964
Sh1 (2747) -----
Sus1 (2895) ACCTTTGCAGCTGT
Sus3 (2738) -----
Consensus (2951)

```

Figure 9f

CGCCAGTCGCCAGTCGCCACAGCCACACCACACACTAGCCGCGGCCGCGGGTAGGAG
CGCGCGCGGCGCGGCGGAACGACCCACCGGTGGCGGCAGCCATGCTGCCCCGAAGCTGA
ACCGCAACGCGAGCATCCGGGACCGCGTCGAGGACACCCTCCACGCGCACCGCAACGAGC
TCGTCGCCCTCCTCTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCGCACCACA
TCCTCGACGCGCTCGACGAGGTCAGGGCTCCGGGGTCCGCGCGCTCGCCGAGGGACCCT
TCCTCGACGTCCTCCGCTCCGCGCAGGAGGCGATCGTGCTGCCGCG

Figure 10

10080114.022102

Maize sequence from SEQ ID NO: 1 in SEQ ID NO: 11

accgcgtgca	ggacacccctc	cacgcgcacc	gcaacgagct	60
acgtgaacaa	gggggaagggc	atccctgcagc	cgcaaccacat	120
tcacaggctc	cgggggcgccg	gcgctagccg	agggaccctct	180
cgacaggagcc	gatcgtgctg	ccgcgcgttcg	tggccatcgc	240
tttgggagta	cgtcccgctc	acgtttcacg	agctcagcgt	300
agtaacctccg	cttcaaggag	gagctgtcgtc	acgggcagaca	360
agcctgaact	cgagccgttc	aatgtctcag	ttccacagcc	420
gaanccggtg	gcagttccctc	aaccgacact	tgtctccaat	480
gcttggagcc	ccctgtggat	ttcctccgtg	gccaccggca	540
tttaatgatg	aatcacaaag	ttggggaggg	ttcagctcgt	600
acttgtcaaa	gctccctgct	gacacacact	actcaacaatt	660
ggggcctgga	gaaagggttg	gggtatacag	caggacatgt	720
ttctagacat	cattcacagg	ccagaccact	ctacccatga	780
ccatgatttt	taacgttgtt	gtggtatccc	ctcatggata	840
taggcttgcc	agacacagga	ggacagatcg	tctatatact	900
aaaatgagat	ggttctccgt	ttaaagaaac	aaggccttga	960
tgtttaccctg	gctgatacca	gatgcaaaag	gaacatcatg	1020
ttagtggaa	acagcatact	tacatattac	gagttccctt	1080
ttangaagt	gatatcaaga	tttgatgtgt	ggccatatct	1140
ctgtgtgtga	aatgtctgct	gaattacaag	gtactccaag	1200
gtgatggaaa	ttctgtggcc	tctattgctat	cttacaagat	1260
ttgctcatgc	ttctgaaaag	actaatgata	cagattcaga	1320
atgagaagta	ccattttctc	tgccagttca	ctgctgatat	1380
atatttatcat	caccagcaca	taccaagaaa	ttgctggaag	1440
atgagagta	tactgccttt	actctgcctg	gtctgtaccc	1500
atcttcgatcc	aaagtccaat	atagttctctc	ctggagatcg	1560
ataccgagaa	ggccaaagca	ctcacctctc	ttcatgggtc	1620
acccggagca	aaacgatgaa	cacattgggc	atctggatga	1680
ttcccatggt	aaagctcgac	aggggtgaag	acataaacag	1740
agtgctgcct	gctgagggag	ctgtgtaaac	ttgtcgtcgt	1800
acaaagccaa	ggagacggga	gagatccggg	agatagagaa	1860
cccacaactt	gttcggcgag	ttccgtgga	ttctgcccca	1920
gcgagctcta	tcgctacatc	gctgatcccc	atgggtgctt	1980
aaagcgttcg	tctcacgcct	gctgagccca	tgacctgttg	2040
ttccatggag	ttccagtgag	atcatagagc	atggcgtctc	2100
accaccggca	acagcgtgtt	aatctgatgg	ccgactcttt	2160
cagatcactg	ggtgaataata	ttctggagcag	ggctcgacgc	2220
ggaagatata	ctcagagagg	ttgatgacac	tggccgggggt	2280
tgtcgaagct	cgagaggctg	gagacgaggg	gctaccttga	2340
tcgcgcagct	ggcgaaagacc	gtgcgcgttg	caattgacca	2400
tgcgactcgc	tagcaccttg	tacaagactg	aaacctgaag	2460
cggcgacgcg	tagcaataaa	aatgtccggg	agctgaactg	2520
tgccagataa	acaaataat	tgaaggcagg	tgggttgccg	2580
actgtattat	gtcagcgtgt	cggtcgcaat	ttcttctgct	2640
aagtgtcgtg	aaatacatca	tattctgttg	acctgtgaaa	2700
cgggcgcg				

Figure 11